

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**

\*\*\*\*\*

# MPSRCH

(TM)

\*\*\*\*\*

Release 3.1A John F. Collins, Biocomputing Research Unit.  
Copyright (C) 1993-1998 University of Edinburgh, U.K.  
Distribution rights by Oxford Molecular Ltd

MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sat Aug 7 19:25:00 1999; MasPar time 1828.51 Seconds  
1515.934 Million cell updates/sec  
Total output not generated.

Title: >US-08-287-669-18  
Description: (4501-5500) from US08287669.seq (6 of 10)  
Perfect Score: 1000  
N.A. Sequence: 4501 GGCTCATCATATATATGAA.....ACCAAAAGAAACCGGAA 5500  
Comp: CGGAGTAGTATTATTTACTT.....TGGTTTCTTTGGGCTTTT

Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 646147 seqs, 138593633 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: emb158  
1:em\_ba1 2:em\_ba2 3:em\_fun 4:em\_htg 5:em\_hum1 6:em\_hum2  
7:em\_in 8:em\_om 9:em\_or 10:em\_ov 11:em\_pat 12:em\_ph  
13:em\_pl 14:em\_ro 15:em\_sts 16:em\_v1  
genbank111  
17:gb\_ba1 18:gb\_ba2 19:gb\_bt1 20:gb\_bt2 21:gb\_in1  
22:gb\_in2 23:gb\_om 24:gb\_ov 25:gb\_pat 26:gb\_ph 27:gb\_pl1  
28:gb\_pl2 29:gb\_pr1 30:gb\_pr2 31:gb\_pr3 32:gb\_ro  
33:gb\_st 34:gb\_sts 35:gb\_sy 36:gb\_un 37:gb\_v1

Statistics: Mean 11.336; Variance 8.769; scale 1.293

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1000	100.0	7653	21	CELCE3A	Caenorhabditis elegans
2	950	95.0	39908	21	CEC48D1	Caenorhabditis elegans
3	936	93.6	31495	19	CEY57H2	Caenorhabditis elegans
4	78	7.8	26788	21	CEL70488	Caenorhabditis elegans
5	73	7.3	299300	20	AC006881	Caenorhabditis elegans
6	70	7.0	36256	21	CEY38A6	Caenorhabditis elegans
7	70	7.0	257817	19	AC006909	Caenorhabditis elegans
8	70	7.0	326074	19	CEY44A6	Caenorhabditis elegans
9	69	6.9	143052	21	CEY17G7B	Caenorhabditis elegans
10	69	6.9	207139	19	CEY17G7	Caenorhabditis elegans
11	68	6.8	12355	19	AC006678	Caenorhabditis elegans
12	67	6.7	22333	21	CELCO2F5	C. elegans cosmid C02F
13	66	6.6	19292	21	CEY76A2A	Caenorhabditis elegans

14	66	6.6	34191	21	CER102	Caenorhabditis elegans
15	66	6.6	245805	20	AC006752	Caenorhabditis elegans
16	66	6.6	269082	19	CEY76A2	Caenorhabditis elegans
17	65	6.5	34700	21	CEC44B9	Caenorhabditis elegans
18	65	6.5	35165	21	CELC56C10	Caenorhabditis elegans
19	65	6.5	38990	21	CEY32B12	Caenorhabditis elegans
20	65	6.5	191857	19	CEY32B12	Caenorhabditis elegans
21	64	6.4	33883	21	CELK03E5	Caenorhabditis elegans
22	64	6.4	37681	19	CEK05C4	Caenorhabditis elegans
23	64	6.4	39184	21	CEY12F11	Caenorhabditis elegans
24	64	6.4	41718	22	CELF16G10	Caenorhabditis elegans
25	64	6.4	43152	21	CELF59B1	Caenorhabditis elegans
26	64	6.4	152878	21	CEY18D10A	Caenorhabditis elegans
27	64	6.4	245805	20	AC006752	Caenorhabditis elegans
28	64	6.4	247332	19	CEY18D10	Caenorhabditis elegans
29	64	6.4	275138	19	CEY54E5	Caenorhabditis elegans
30	64	6.4	31957	19	AC006782	Caenorhabditis elegans
31	63	6.3	20836	21	CEY54F11	Caenorhabditis elegans
32	63	6.3	32205	21	CEY11D9	Caenorhabditis elegans
33	63	6.3	44726	21	CELF09E5	Caenorhabditis elegans
34	63	6.3	119562	19	AC006779	Caenorhabditis elegans
35	63	6.3	140702	20	AC006888	Caenorhabditis elegans
36	63	6.3	291821	19	CEY48E1	Caenorhabditis elegans
37	62	6.2	33511	21	CEYK10I10	Caenorhabditis elegans
38	62	6.2	43152	21	CELF59B1	Caenorhabditis elegans
39	62	6.2	75073	21	CEY48A6B	Caenorhabditis elegans
40	62	6.2	110000	19	CEY39E4	Caenorhabditis elegans
41	62	6.2	296899	19	CEY48A6	Caenorhabditis elegans
42	61	6.1	26542	21	CEM18	Caenorhabditis elegans
43	61	6.1	36120	21	CELF56D1	Caenorhabditis elegans
44	61	6.1	144763	19	CEY40D7	Caenorhabditis elegans
45	61	6.1	331326	19	AC006802	Caenorhabditis elegans

## ALIGNMENTS

RESULT	LOCUS	DEFINITION	1	CELCE3A	7653 bp	DNA	INV	23-FEB-1994
				Caenorhabditis elegans cell death protein (ced-3) gene, complete cds.				
	ACCESSION			L29052				
	VERSION			g456416				
	KEYWORDS			L29052.1 GI:456416				
	SOURCE			cell death protein; interleukin-1 beta converting enzyme.				
	ORGANISM			Caenorhabditis elegans (strain N2) DNA.				
	REFERENCE			1 (bases 1 to 7653)				
	AUTHORS			Yuan, J., Shahan, S., Ledoux, S., Ellis, H.M. and Horvitz, H.				
	TITLE			The C. elegans cell death gene ced-3 encodes a protein similar to mammalian interleukin-1b-converting enzyme				
	JOURNAL			Cell 75, 641-652 (1993)				
	MEDLINE			94061982				
	FEATURES			Location/Qualifiers				
	source			1..7653				
				/organism="Caenorhabditis elegans"				
				/strain="N2"				
	exon			/db_xref="taxon:6239"				
				2167..2366				
				/gene="ced-3"				
				/number=1				
	gene			join(2332..2366,2430..2575,2854..3107,4303..4634,5547..5760,5815..5942,6298..6537,7013..7075)				
				/gene="ced-3"				
	CDS			join(2332..2366,2430..2575,2854..3107,4303..4634,5547..5760,5815..5942,6298..6537,7013..7075)				
				/gene="ced-3"				
				/note="codes for a protein similar to mammalian interleukin-1b-converting enzyme"				
				/codon_start=1				
				/product="cell death protein"				

/protein\_id="AAA27982.1"  
 /db\_xref="pid:g456417"  
 /db\_xref="gi:456417"  
 /translation="MRQDRRLRNIMFSSHLKVDLEILVLIKQVLNSDGMV  
 NSCGTVREKREIVKAVRGDVAFAFYDALRSTGHEGLAEVLEPLARSVDNAVEF  
 ECPMSPASRRALSAPGTSPTVRHDSVSVSFTSYQDIYSRARSRSRALHS  
 SDRNPSPPVNAFPSPSSANSFTGCSLSGSSSRNRSFSKASGPTQYIFHEEDMN  
 FVDAPTISRYNDEKTYRNFSSPRGMLIINNEHFOMPTRNKGADKDLNLFRCM  
 GYTVCKDNLTDGKMLLTIRDFAKHSHGSDAILVILSHGEENVILGVDDIPITSTHEI  
 YDLNANARPLANKPIVFOACRGERDNGFPVLDSDVGVPAFLRRGWDNRDGLF  
 NFGCVPRVQVQVWRKPKSQADILIRITTAQVSWRNSARGSNFIOACVEVSTHAK  
 DMDVVELLTVEVNRKVKACGFGTSGSNIKKOMPETSRLLKKFYFNPPEARNAV"  
 2367..2429

intron  
 /gene="ced-3"  
 /number=1

exon  
 2430..2575  
 /gene="ced-3"

intron  
 /number=2  
 2576..2853

intron  
 /gene="ced-3"  
 /number=2

exon  
 2854..3107  
 /gene="ced-3"

intron  
 /number=3  
 3108..4302

intron  
 /gene="ced-3"  
 /number=3

exon  
 4303..4634  
 /gene="ced-3"

intron  
 /number=4  
 4635..5546

intron  
 /gene="ced-3"  
 /number=4

exon  
 5547..5760  
 /gene="ced-3"

intron  
 /number=5  
 5761..5814

intron  
 /gene="ced-3"  
 /number=5

exon  
 5815..5942  
 /gene="ced-3"

intron  
 /number=6  
 5943..6297

intron  
 /gene="ced-3"  
 /number=6

exon  
 6298..6537  
 /gene="ced-3"

intron  
 /number=7  
 6538..7012

intron  
 /gene="ced-3"  
 /number=7

exon  
 7013..7652  
 /gene="ced-3"

intron  
 /number=8

exon

BASE COUNT 2429 a 1455 c 1271 g 2498 t  
 ORIGIN

Query Match 100.0%; Score 1000; DB 21; Length 7653;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 1000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 4501 GCCTCATATAATATGAACACTTTGACGAGATGCCAACAGGAAATGGTACCAAGGCCG 4560  
 QY 4501 GCCTCATATAATATGAACACTTTGACGAGATGCCAACAGGAAATGGTACCAAGGCCG 4560  
 Db 4561 ACAAGGACAATCTTACCAATTTGTTTCAGATGCGATGGCTATACGGTTATTTGCAAGGACA 4620  
 QY 4561 ACAAGGACAATCTTACCAATTTGTTTCAGATGCGATGGCTATACGGTTATTTGCAAGGACA 4620  
 Db 4621 ATCTGACGGGAGGTACGGGAAATATATATACCAACCGGAAATTTGCCATTTTCGG 4680  
 QY 4621 ATCTGACGGGAGGTACGGGAAATATATATACCAACCGGAAATTTGCCATTTTCGG 4680

RESULT 2  
 LOCUS C8C48D1 39908 bp DNA INV 23-NOV-1998  
 DEFINITION Caenorhabditis elegans cosmid C48D1, complete sequence.  
 ACCESSION Z81049  
 NID g1627677  
 VERSION Z81049.1 GI:1627677  
 KEYWORDS HRG.  
 SOURCE Caenorhabditis elegans.  
 ORGANISM Caenorhabditis elegans  
 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;  
 Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.  
 REFERENCE 1 (bases 1 to 39908)  
 AUTHORS Burton, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-OCT-1996) Louis, MO 63110, USA. E-mail:  
 jes@sanger.ac.uk or rw@nematode.wustl.edu

/gene="F36G9.9"  
 /codon\_start=1  
 /protein\_id="CAB04339.1"  
 /db\_xref="PID:el346505"  
 /db\_xref="PID:g3876818"  
 /db\_xref="GI:3876818"  
 /translation="MCIDMSGPDWYFAMHFSALVTPVNISSIMILFCQRLSSLR  
 WLLVQIFQMSIDPSLNGVLPVFPSPGIRGPGVTLIFQKFGFTSTEAOCILV  
 VPDQVARSVEFLRLRYQAILPSGPHKLSIFSVLLSIQVFLITMLISFKLA  
 LIWSSRLKSIQISLTKRMHLQILKSLCOOIIIVPIAFYPIIIVVPLMISIPNS  
 OLSFISLISLSTYFTFGTSLMLYFNPHYROWVISAVRNPMNTSTALTSKFLVARER  
 SNFAGRNVSAPI.  
 complement(15178..16575)  
 /gene="F36G9.8"  
 complement(join(15178..15374,15422..15503,15559..16011,  
 16224..16367,16423..16575))  
 /gene="F36G9.7"  
 /codon\_start=1  
 /protein\_id="CAB04337.1"  
 /db\_xref="PID:el346503"  
 /db\_xref="PID:g3876816"  
 /db\_xref="GI:3876816"  
 /db\_xref="SPTREMBL:O45476"  
 /translation="MPIEVPDPIYIGMHFSAMITTPVNISSIMILFCQRLASLR  
 WLLVQVQMSIDPSLNGVLPVFPSPGIRGPGVTLIFQKFGFTSTEAOCILV  
 IVSLVTVAGSVELFLRYQAILPSGPHKLSIFSVLLSIQVFLITMLISFKLA  
 IPDQVARSVEFLRLRYQAILPSGPHKLSIFSVLLSIQVFLITMLISFKLA  
 LIWSSRLKSIQISLTKRMHLQILKSLCOOIIIVPIAFYPIIIVVPLMISIPNS  
 OLSFISLISLSTYFTFGTSLMLYFNPHYROWVISAVRNPMNTSTALTSKFLVARER  
 SNFAGRNVSAPI.  
 complement(16755..18686)  
 /gene="F36G9.6"  
 complement(join(16755..16798,16899..17108,17487..17614,  
 17678..18017,18075..18108,18600..18686))  
 /gene="F36G9.5"  
 /codon\_start=1  
 /protein\_id="CAB04338.1"  
 /db\_xref="PID:el346504"  
 /db\_xref="PID:g3876817"  
 /db\_xref="GI:3876817"  
 /db\_xref="SPTREMBL:O45477"  
 /translation="MTSGLIVHWSLHLLHRRHLVGSIOFLSERTNTKMKIRYALIS  
 ITNILLGVALFLVGRINDNSGTLDPSPVPCIMVAVLIPIDILYWKHFDFA  
 LNFVLPFRPSIRSKNEQVOMKEDSKNRSSKLMKFKVIRIIVLVILGTF  
 SALYVHTSIHTSGENPYPIIYISYFGLFALFYFKIHLFSIFNLINFEQLFS  
 PIPFNEAIYVYLNKPFQHSFPIYELCYLTHYTNLTCTYSIFVFNVSFSEKVCXK  
 LNVI.  
 complement(19366..21512)  
 /gene="F36G9.4"  
 remainder of annotations omitted.

Query Match 4.2%; Score 19; DB 21; Length 37704;  
 Best Local Similarity 100.0%; Pred. No. 3.38e+00;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 28373 ATTGATCCCGGCAAAAAT 28391  
 Cp 7429 ATTGATCCCGGCAAAAAT 7411

RESULT 10  
 LOCUS SCU43503 38590 bp DNA PLN  
 DEFINITION Saccharomyces cerevisiae chromosome XVI cosmid 8209/8002.  
 ACCESSION U43503 U00094  
 NID g1163087  
 VERSION U43503.1 GI:1163087  
 KEYWORDS Schizosaccharomyces pombe C18B11.10 homolog; NIP29; Aspergillus  
 oryzae ribonuclease T2 homolog; MEI5; H.sapiens GT197 EST homolog;  
 DBP1; S.kluuyverii k-ORF1 homolog; IDI1; C.elegans CF4366.4 product  
 homolog; BEK3; E.coli 2-hydroxyacid dehydrogenase homolog; trNAMet;

SOURCE  
 ORGANISM  
 CARI; S.cerevisiae Pho81p homolog; Clostridium pasteurianum protein  
 homolog.  
 baker's yeast.  
 Saccharomyces cerevisiae  
 Eukaryotae; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;

REFERENCE  
 AUTHORS  
 TITLE  
 Nucleotide sequence of the Saccharomyces cerevisiae arginase gene  
 (CARI) and its transcription under various physiological conditions  
 J. Bacteriol. 160 (3), 1078-1087 (1984)

JOURNAL  
 MEDLINE  
 REFERENCE  
 AUTHORS  
 Anderson, M.S., Muehlbacher, M., Street, I.P., Proffitt, J. and  
 Poultter, C.D., Isopentenyl diphosphate:dimethylallyl diphosphate isomerase. An  
 improved purification of the enzyme and isolation of the gene from  
 Saccharomyces cerevisiae  
 J. Biol. Chem. 264 (32), 19169-19175 (1989)

JOURNAL  
 MEDLINE  
 REFERENCE  
 AUTHORS  
 Jamieson, D.J. and Beggs, J.D.  
 A suppressor of yeast spp81/ded1 mutations encodes a very simil  
 putative ATP-dependent RNA helicase  
 Mol. Microbiol. 5 (4), 805-812 (1991)

JOURNAL  
 MEDLINE  
 REFERENCE  
 AUTHORS  
 Zheng, F., Cerlione, R. and Bender, A.  
 Control of the yeast bud-site assembly GTPase Cdc42. Catalysis  
 guanine nucleotide exchange by Cdc24 and stimulation of GTPase  
 activity by Bem3  
 J. Biol. Chem. 269 (4), 2369-2372 (1994)

JOURNAL  
 MEDLINE  
 REFERENCE  
 AUTHORS  
 Bussey, H., Storms, R.K., Ahmed, A., Albermann, K., Allen, E.,  
 Benes, V., Botstein, D., Bowman, S., Bruckner, M., Carpenter, J.,  
 Cherry, J.M., Chung, E., Churcher, C., Coster, F., Davis, K.,  
 Davis, R.W., Dietrich, F.S., Dilius, H., Dipaolo, T., Dubois, E.,  
 Dusterhoft, A., Duncan, M., Floeth, M., Fortin, N., Friesen, J.D.,  
 Fritz, C., Goffeau, A., Hall, J., Hebling, U., Heumann, K., Hilbert, H.,  
 Hillier, L., Hunkeler, Smith, S., Hyman, R., Johnston, M., Kaman, S.,  
 Kleene, K., Komp, C., Kurdi, O., Lashkari, D., Lew, H., Lin, A., Lin, D.,  
 Louis, E.J., Marathe, R., Messenguy, F., Mewes, H.W., Mirtipati, S.,  
 Mostl, D., Muller-Auer, S., Namath, A., Nentwich, U., Oefner, P.,  
 Pearson, D., Petel, F.X., Pohl, T.M., Purnelle, D., Schafer, M.,  
 Schaffner, M., Scherrens, B., Schramm, S., Schroeder, M., Sdicu, A.M.,  
 Tettelin, H., Urrestarazu, L.A., Ushinsky, S., Vierendeels, F.,  
 Vissers, S., Voss, H., Walsh, S.V., Wambutt, R., Wang, Y., Wedler, E.,  
 Wedler, H., Winnett, E., Zhong, W.W., Zollner, A., Vo, D.H. and Hani, J.  
 The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI  
 Nature 387 (6632 Suppl), 103-105 (1997)

JOURNAL  
 MEDLINE  
 REFERENCE  
 AUTHORS  
 Schlensstedt, G. and Silver, P.A.  
 Unpublished  
 (bases 1 to 38590)

JOURNAL  
 MEDLINE  
 REFERENCE  
 AUTHORS  
 Hall, J., Ahmed, A., Bussey, H., Fortin, N., Friesen, J.D.,  
 Storms, R.K., Vo, D.H., Wang, Y. and Winnett, E.  
 The sequence of Saccharomyces cerevisiae chromosome XVI left arm  
 Unpublished  
 (bases 1 to 38590)

JOURNAL  
 MEDLINE  
 REFERENCE  
 AUTHORS  
 Weber, L. and Byers, B.E.  
 mei5, a novel meiotic mutation  
 Unpublished (1992)

JOURNAL  
 MEDLINE  
 REFERENCE  
 AUTHORS  
 Bussey, H.  
 Direct Submission  
 Submitted (15-DEC-1995) Howard Bussey, McGill University, Biology,  
 1205 Dr. Penfield Ave., Montreal, Quebec H3A 1B1, Canada

JOURNAL  
 MEDLINE  
 REFERENCE  
 AUTHORS  
 Jia, Y. and Cherry, J.M.  
 Direct Submission

**COMMENT**

Curated by:

All CDS of 100 or more codons have been analyzed. CDS that are overlapped by larger CDS are not included. Cosmid 8209/8002 is overlapped at the beginning by cosmid 9545, and at the end by cosmid 8059.

**FEATURES**

misc\_feature

```

gene
353. .3043
/note= overlaps cosmid 9343
/gene="YPL126W"
CDS
353. .3043

```

/gene="IPL12BW"  
/note="similar to protein C18B11.10 encoded on chromosome  
I of Schizosaccharomyces pombe, Swiss-Prot Accession  
number O09715"

```
/codon_start=1
/product=Vp112
```

```

/product = ip1r2wp
/protein_id = "AAB6236.1"
/db_xref = "P016308"
/db_xref = "GI:116308"
/translation = "MTQSLGIEQYKLSVYSGGKPALNNLSITGNKNIARLSQDQRNY
IIPNQIKVSYETQCVYTKLFKFNANSLISGIFQEERENNESSYKILGLDITVPQOE
DAHLINVFYNGHVIYLVNKGKLVESPKEFKISLADEKLANVPHSEGNYRILITFKDP
SQAHNLSQRILAUFTDDPAKQFVPAQEAQHWNVILSNISGKLAHMCMDKSTK
DHEKHSVSWSLFDDVNSLFSPLGSLTSSTQSLSYNISYSMAIDNNQQLAVGFA
SGVISTSLADQLIRLLKWHIDISLSFSHDGSLTSGGWEKVSMLQLETNSQOFL
PRUNGIIIDCVLPGCGNYYSITLQNTNNNSDYQFLLNASDLTSLKLSINGPLPVF
NSTIKHIQTP ISAMNTKNSNYSITSLNHSKKOSRKLIKSRQDFTVEINPINKNLY
FPHISAVQIFDFPVKNQSNQYVLTSCVNNSMGKVPRELNLQDPIITDLKFTKDGQWMI
TYELIEVPNDLSSKDLTHLAFWTKNDNETWNKLTKVINPHGISVYPTKILSPRS
VSNQCLTADNNGGKGFSPFSDHESNWCCLKISLPFNKHSVNSLSAWSQGSGLIFH
GFDDKQLIDDFPKFESLETNTKTSFEEDSQTQVTLKINDINLIVATRTLLNAIN
LLRGVINSFDLTPFYNGVYKNGHMWLTICDERTGNIALVINQQTUDJGQYLTNK
SRIIIFPDSOLTKLGNFTTHEYKISLWGNVYDTDFIPLDIESTLGVYGVTTQYQLNSD
FINGEKILGLSVNTITTSAGNSDIFSAQLHKLRSRGGKSDTRKNTDNDNDEEDIALE
FINGEKKDKLVNNNSFTSNFDNTONVQMTDFEDRVMKVIT"

```

ene  
CDS

```

3531. 7023
/ gene="YPL125W"
/ codon_start=1
/ product="Ypl125wp"
/ protein_id="AB568237.1"
/db_xref="PIR:g1163089"
/db_xref="GI:1163089"

```

/translation="\*\*MASSINELNVLQVLEQASNPQHIRSDQVKLAEQQLRBQWETQAGF  
 HYLLQSLIQLNLSNSLQIRMLAVLQVFKNGVDKFWKRSTRINAIPDKERKASIRGRUFEMID  
 EQNNQICLQNAQASARIARLUDLPVPEMTLFDENLUNDEIIRKDSKSYKIINLHMILHINO  
 IVKVLTRIGRCPAQOSKVPILFIVIRLYQSEEWTTSSNLNDEYDSLSQVLEK  
 ALKVLARIICEGVRDPTQSGDFTKLSVSHFEMLSIHNHFNKFDIYKFKICLGLK  
 LVNVLVGPANFILLPCSTOITLITRFLIDKAPKPVYRSENDSVTDQWEOQTARIGLL  
 ILKRVNFTHKGAJLTKARSDKLTIDASINTFELNENLTIDVDTDMEWYLRRLR  
 PTELENNWDFPEWIMEQWATSYEYOIRPCAENVFODLANTFSELLVPLYLKAKIENDA  
 SKLSUNDEWDLRKDAIYASFQLSASVSEWDFDRLLIQVFLPEATNTNISGDELRII  
 RKRVALIINLFWSTKCYSEKSLCYKLFNTDFDEDDKQVLVLTQVTRVITNMSDWNFN  
 KDTFPFLFTEINVHLLKRLPVSVLTRTLYLNTLSDIIIOQTKPLSRIDLVLVEIQLI  
 IPNLWATINNASEAFLANALRLRLNLSYSGSQSLHTWDAIPVALCALDSVPEIQLQ  
 QLLSDEGYELWGLMLQNFSSHQDEQDFKVELVPFLKYEIETHETLPTLLETKIISYQ  
 LILNPYDTSNNTFODIFKMSYKLLKREDSPQVLEIWEIETLISNESDYENLLIOLK

FFYETGVLSALFDPAIFLEAPSPYLCSSQIIQIARIYSVNPDALMTFLAVYHDNLPSTS  
ENARMPSSIRKTSKDOTYSVNVKLTGIVCFRDFDPKFKVHGLSSLLRTGL  
PLTPFTSSIASLWLEENLEETNMGDCXKHYLANDIVTSQISAFHPLTAEQURLHQ  
KKNDDPVHNIISLKDFISQSMEYLESHGVRYQEFLKINPSSLLENQMFSLSTQPEA  
R<sup>pp</sup>

```

gene
6998..7659
/gene="NIP29"
/db_xref="SGD:L0001253"
6998..7659
/gene="NIP29"
/notes="YPL124W"
/codon_start=1
/db_xref="SGD:L0001253"
/product="Nip29p: Nuclear
import protein"
/protein_id="AAB68238.1"
/db_xref="PID:g1163090"
/db_xref="GI:1163090"

```

gene	complement(7784..9088)
CDS	complement(7784..9088)

```

/codon_start=1
/product="Yp1123cp"
/protein_id="AAB68239.1"
/db_xref="PID:g1163091"
/db_xref="GI:1163091"
/translation="MLKNLHSLLL
CFEYPGGIFLQFVYFPKNDI
NRSLQIDDDVYLLHDKDKFNNDI
GTCTIIRPECVTEWCANSVDRKR
YSLEQIALSKFEFGKKVIGCD
CKDGIKFPKGYPVTFRRPNKG
ANYELIKSPGYNLRTNQGFCDI
YSGNYWNGDTPRRNQSPISV
complement(9369..10910)
/gene="TFB2"
complement(9369..10910)
/gene="TFB2"

```

...  
Note: remainder of annotations omitted.

```
Query Match      4.2%; Score 19; DB 28; Length 38590;
Best Local Similarity 100.0%; Pred. No. 3.38e+00;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Dbb 4612 ATGCTTCTATCAACAAAT 4630
      |||||
Ov 7343 ATGCTTCTATCAACAAAT 7361

```

RESULT	11				
LOCUS		HS657J8	98954 bp	DNA	PRI 11-DEC-1998
DEFINITION		Human DNA sequence from clone 657J8 on chromosome Xq26.1-26.3 Contains GSS. complete sequence.			

NID 93980437  
VERSION AL034407.1 GI:3980437  
KEYWORDS HTG.  
SOURCE human

ORGANISM Homo sapiens  
 YOROTA Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 98954)  
 AUTHORS Grafham,D.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-DEC-1998) Sanger Centre, Hinxton, Cambridgeshire

/protein\_id="AA27982.1"  
/db\_xref="PID:g456417"  
/db\_xref="GI:456417"  
/translation="MRQDRSLRLNMFSSHLKVDLELVLIKQVLSNDGDM  
NSCGTVREKREIVKAVQRGDVDFADALSTGHEGLAEVLEPLKSVDSNAVEF  
ECSPYASHRSRALPAGTSPTRVHRSVSVSFTSYQDIYSRARSRSRALHS  
SDHNTSPVPNPAPPSPSSNSFTGCSLGYSSRNRSFKAAGTQYIFHEEDMN  
FVDAPTISKDLTIRNFSSPRGMCLIIINNEHFMPTNGTKADKONLNLPRCM  
GYTVICKDLTGRGMLTIRDFAKHSHGSDSALLVLSHGEENVIIIGVDDIPISTHEI  
YDLNANAPRLANKPKIVQACRGERDNGFPVLDSDVGPAPFLRGRWDRDGLF  
NFGCVRPQVQWRKKPSQADILIRIATTAQVSWNSARGSWFLOACEVSETHAK  
DMDVELLTEVNNKVCAGFGTSGSNILKOMPENTSRLLKKFYFNPARNASV"  
2367..2429  
/gene="ced-3"  
/number=1  
2430..2575  
/gene="ced-3"  
/number=2  
2576..2853  
/gene="ced-3"  
/number=2  
2854..3107  
/gene="ced-3"  
/number=3  
3108..4302  
/gene="ced-3"  
/number=3  
4303..4634  
/gene="ced-3"  
/number=4  
4635..5546  
/gene="ced-3"  
/number=4  
5547..5760  
/gene="ced-3"  
/number=5  
5761..5814  
/gene="ced-3"  
/number=5  
5815..5942  
/gene="ced-3"  
/number=6  
5943..6297  
/gene="ced-3"  
/number=6  
6298..6537  
/gene="ced-3"  
/number=7  
6538..7012  
/gene="ced-3"  
/number=7  
7013..7652  
/gene="ced-3"  
/number=8

Db	4681	CGGAAATGTGGCCCGCGTCTCGACACGACAAATTTGTGTAAATGCAAAATGTATAAT	4740
Qy	4681	CGGAAATGTGGCCCGCGTCTCGACACGACAAATTTGTGTAAATGCAAAATGTATAAT	4740
Db	4741	TTTGCAAAAACAAAATTTTGAACCTTCGCGGAAAATGATTACCTAGTTTCGAAATTTTC	4800
Qy	4741	TTTGCAAAAACAAAATTTTGAACCTTCGCGGAAAATGATTACCTAGTTTCGAAATTTTC	4800
Db	4801	GTGTTTTCCGGCTACATATGTTTTCTTAGTTTTCTATATAATTTTGATGTAATAA	4860
Qy	4801	GTGTTTTCCGGCTACATATGTTTTCTTAGTTTTCTATATAATTTTGATGTAATAA	4860
Db	4861	ACCGTTTGTAAATTTTCAGACAAATTTTCGCATACAAAATTTGATAGCAGAAATCAAT	4920
Qy	4861	ACCGTTTGTAAATTTTCAGACAAATTTTCGCATACAAAATTTGATAGCAGAAATCAAT	4920
Db	4921	TTCTGAATTTTCAAAATATCCAAAATGCACAAATTTAAATTTGTGAAATTTGGCAAC	4980
Qy	4921	TTCTGAATTTTCAAAATATCCAAAATGCACAAATTTAAATTTGTGAAATTTGGCAAC	4980
Db	4981	GGTGTTCATATGAATGATTTTAAACCTTTTAAACCTTCGCGGAAAAGCAATAA	5040
Qy	4981	GGTGTTCATATGAATGATTTTAAACCTTTTAAACCTTCGCGGAAAAGCAATAA	5040
Db	5041	AAATCAAAACACGTCACAAATTCAAAATTCAAAAGTTTATTCATCCGATTTGTTTATTTTG	5100
Qy	5041	AAATCAAAACACGTCACAAATTCAAAATTCAAAAGTTTATTCATCCGATTTGTTTATTTTG	5100
Db	5101	CAAAATTTGAAAATATCATGAAGGATTTAGAAAGTTTATTAACATTTTCTAGATTTT	5160
Qy	5101	CAAAATTTGAAAATATCATGAAGGATTTAGAAAGTTTATTAACATTTTCTAGATTTT	5160
Db	5161	TCAAAATTTTAAACAAATCGAGAAAAGAAATGAAAATCGAATTTTAAATATATCC	5220
Qy	5161	TCAAAATTTTAAACAAATCGAGAAAAGAAATGAAAATCGAATTTTAAATATATCC	5220
Db	5221	ACAGCTTCGAGAGTTTGAATTTACAGTACTCTTAAAGGCGACACCCATTTGCATTTG	5280
Qy	5221	ACAGCTTCGAGAGTTTGAATTTACAGTACTCTTAAAGGCGACACCCATTTGCATTTG	5280
Db	5281	ACCAAAATTTGTCGTGCGAGACAGGACCGTACCGTATTTTGTGCAAAAATTTGCACCAT	5340
Qy	5281	ACCAAAATTTGTCGTGCGAGACAGGACCGTACCGTATTTTGTGCAAAAATTTGCACCAT	5340
Db	5341	TGGACAAATAAACCCTTCTATCACCAAAAGTAAATTTGAAAATCTTCGAAAAGCCAAA	5400
Qy	5341	TGGACAAATAAACCCTTCTATCACCAAAAGTAAATTTGAAAATCTTCGAAAAGCCAAA	5400
Db	5401	ATTCAAAAATTTGCGAATTTTCGATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT	5460
Qy	5401	ATTCAAAAATTTGCGAATTTTCGATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT	5460
Db	5461	AAATCAATTTTTCGAAAATATACAAAAGAACCCGAAAA	5500
Qy	5461	AAATCAATTTTTCGAAAATATACAAAAGAACCCGAAAA	5500

RESULT	2	CEC48D1	39908 bp	DNA	INV	23-NOV-1998
LOCUS		Caenorhabditis elegans	cosmid C48D1			complete sequence.
DEFINITION		281049				
ACCESSION		91627677				
NID		281049.1	GI:1627677			
VERSION		HTG.				
KEYWORDS		Caenorhabditis elegans.				
SOURCE		Caenorhabditis elegans				
ORGANISM		Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;				
REFERENCE		Rhabditina; Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.				
AUTHORS		Burton, J.				
TITLE		1 (bases 1 to 39908)				
JOURNAL		Direct Submission				
		Submitted (21-OCT-1996) Louis, MO 63110, USA. E-mail:				
		jesssanger.ac.uk or rw@nematode.wustl.edu				

Query Match	100.0%;	Score 1000;	DB 21;	Length 7653;
Best Local Similarity	100.0%;	Pred. No. 0.00e+00;		
Matches 1000;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps	0;			
4501	GCCTCATCAATAAATGAACACATTTGAGCAGATGCCAACACGGAATGGTACCAAGGCCG	4560		
4501	GCCTCATCAATAAATGAACACTTTGAGCAGATGCCAACACGGAATGGTACCAAGGCCG	4560		
4561	ACAAGGACAAATCTTACCAATTTGTTACAGATGCGCTATACGGTATTTGCAAGGACA	4620		
4561	ACAAGGACAAATCTTACCAATTTGTTACAGATGCGCTATACGGTATTTGCAAGGACA	4620		
4621	ATCTGACGGGAAGGTACGGGAAATATATATACCAAAACGCGAAATTTGCCATTTTGGC	4680		
4621	ATCTGACGGGAAGGTACGGGAAATATATATATACCAAAACGCGAAATTTGCCATTTTGGC	4680		



